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TECH CENTER 1600/2900

P#18

1600

RAW SEQUENCE LISTING

DATE: 05/14/2003

PATENT APPLICATION: US/09/676,249C

TIME: 08:07:42

Input Set : A:\3153.162.PC10555A.Substitute.Seq.ST25.txt

Output Set: N:\CRF4\05142003\I676249C.raw

mhp3

3 <110> APPLICANT: King, Kendall W.
 4 Madura, Rebecca A
 5 Rosey, Everett L
 7 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA HYOPNEUMONIAE

8 GENE AND USES THEREOF

10 <130> FILE REFERENCE: 3153.00162/PC10555
 12 <140> CURRENT APPLICATION NUMBER: US 09/676,249C
 13 <141> CURRENT FILING DATE: 2000-09-29
 15 <150> PRIOR APPLICATION NUMBER: US Prov. 60/156,602
 16 <151> PRIOR FILING DATE: 1999-09-29
 18 <160> NUMBER OF SEQ ID NOS: 42
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1692
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Mycoplasma hyopneumoniae
 27 <400> SEQUENCE: 1

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 30 tcatcgtaat taaaacaatt aattaggaga acaactatga aaaaaaagat aaaatgaaat 120
 32 aaattttcttg gcttaggctt agttttttccg ctttcagcaa tcgcgacaat ctctgccgga 180
 34 tgttgggata aagaacaac taaagaagaa aaatcagccg ataatacaaa taagcaaatc 240
 36 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 300
 38 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggacg 360
 40 gtaaatgata attcatttaa ccaatcaagt tgagaggcaa ttcaacaact tggcgctctt 420
 42 actggaggty agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 480
 44 tcaacttgcta ataccaacaa aaatgtttga gtactttctg gttttcaaca cgggtgatgcg 540
 46 ttcacaagat gattaaaaat cctgaaaat aagcaattat ttactgaaaa aaatattatc 600
 48 atactcggaa ttgactgaac tgatactgaa aatgtaatc caacaggctg atatattaat 660
 50 ttaacctata aaactgaaga agccggatga cttgcaggat atgcgaatgc ttccctttttg 720
 52 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 780
 54 tcgccagctg taactgattt tatcgctggt tatctagccg gaattaaagc ttgaaatcta 840
 56 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggggtt 900
 58 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 960
 60 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcgatat aatcgcaaac 1020
 62 caaaatgatc gttatctcat tgggtgttgac accgaccaat cacttgttta taaaaaact 1080
 64 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 1140
 66 agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa 1200
 68 aaaagtgcga ccgtttatct tggaaattaa gacaggtttg tcgatattgc tgatacttct 1260
 70 ttagaaggca atgataaaaa actcgcaact gaagcattt ctgaagctaa aaaagaattt 1320
 72 gaagaaaaaa ctaagacaat tcctgccgaa gaagttcgta aaactttaga aattccggaa 1380
 74 atgcctgata aacaacctga taagcaacag gaaagcttag acaaaactaat taccgatatt 1440
 76 aataaaaaatt aagtaagaaa aaataacaat tttttaacat tatatctttt tttagagatt 1500
 78 aattttcttc taatttagtt taatttaata taaaattata ttaaattaaa aaaataaaaa 1560

P.6

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80 atccggacta tttttgttcc ggatttttta tttttgtgtt actatttaaat ataataataa 1620
82 atcaggatta tgcaattgaa tttattcaag tctcgaaaaa atttggcagt ttttatgcca 1680
84 attacaaaaat ag 1692
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 451
89 <212> TYPE: PRT
90 <213> ORGANISM: Mycoplasma hyopneumoniae
92 <400> SEQUENCE: 2
94 Met Lys Lys Lys Ile Lys Trp Asn Lys Phe Leu Gly Leu Gly Leu Val
95 1 5 10 15
98 Phe Pro Leu Ser Ala Ile Ala Thr Ile Ser Ala Gly Cys Trp Asp Lys
99 20 25 30
102 Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile
103 35 40 45
106 Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu
107 50 55 60
110 Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met
111 65 70 75 80
114 Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln
115 85 90 95
118 Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu
119 100 105 110
122 Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu Gly Lys Tyr Ser
123 115 120 125
126 Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln
127 130 135 140
130 His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln
131 145 150 155 160
134 Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp
135 165 170 175
138 Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys
139 180 185 190
142 Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu
143 195 200 205
146 Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile
147 210 215 220
150 Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu
151 225 230 235 240
154 Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys
155 245 250 255
158 Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp
159 260 265 270
162 Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro
163 275 280 285
166 Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp
167 290 295 300
170 Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp
171 305 310 315 320
174 Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile

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Input Set : A:\3153.162.PC10555A.Substitute.Seq.ST25.txt

Output Set: N:\CRF4\05142003\I676249C.raw

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175          325          330          335
178 Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr
179          340          345          350
182 Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys
183          355          360          365
186 Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile
187          370          375          380
190 Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala
191 385          390          395          400
194 Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro
195          405          410          415
198 Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys
199          420          425          430
202 Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu Ile Thr Asp Ile
203          435          440          445
206 Asn Lys Asn
207          450

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210 <210> SEQ ID NO: 3

211 <211> LENGTH: 1263

212 <212> TYPE: DNA

213 <213> ORGANISM: Artificial Sequence

215 <220> FEATURE:

216 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in vitro

217 expression

219 <400> SEQUENCE: 3

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220 atgtgggata aagaaacaac taaagaagaa aaatcagccg ataatcaaaa taagcaaadc 60
222 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 120
224 aaagctgatg caaacaacaa ttttgggcta aatatggcaa ttgtaacgcg tggtggaacg 180
226 gtaaatagata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240
228 actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300
230 tcaacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cggatgatgc 360
232 ttcacaagat ggttaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 420
234 atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggctg atatattaat 480
236 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg 540
238 gcaaaaaaat tccaagtga tccaactaaa agatcagcaa ttgttatcgg tggtgggatt 600
240 tcgccagctg taactgattt tatcgtcgtt tatctagccg gaattaaagc ttggaatcta 660
242 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggtgtt 720
244 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780
246 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 840
248 caaaatgatc gttatctcat tgggtgtgac accgaccaat caattgttta taaaaaaact 900
250 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960
252 agtgatttat atacaaaaaa atcaaattca agaaatttag ccggcctttg atttggtaaa 1020
254 aaaagtgcga ccgtttatct tgggaattaa gacaggtttg tcgatattgc tgatacttct 1080
256 ttagaaggca atgataaaaa actgcgaact gaagccattt ctgaagctaa aaaagaattt 1140
258 gaagaaaaaa ctaagacaat tcctgcgaa gaagtctgta aaactttaga aattccggaa 1200
260 atgcctgata aacaacctga taagcaacag gaaagcttag acaaacttaa ttaccgatat 1260
262 taa

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265 <210> SEQ ID NO: 4

266 <211> LENGTH: 423

RAW SEQUENCE LISTING

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Input Set : A:\3153.162.PC10555A.Substitute.Seq.ST25.txt

Output Set: N:\CRF4\05142003\I676249C.raw

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267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in
272     vitro expression
275 <220> FEATURE:
276 <221> NAME/KEY: MISC_FEATURE
277 <222> LOCATION: (1)..(423)
278 <223> OTHER INFORMATION: Xaa is any amino acid
280 <400> SEQUENCE: 4
282 Met Trp Asp Lys Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln
283 1          5          10          15
286 Asn Lys Gln Ile Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu
287          20          25          30
290 Arg Lys Ser Glu Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe
291          35          40          45
294 Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn
295          50          55          60
298 Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu
299 65          70          75          80
302 Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu
303          85          90          95
306 Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu
307          100         105         110
310 Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro
311          115         120         125
314 Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile
315          130         135         140
318 Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn
319 145         150         155         160
322 Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn
323          165         170         175
326 Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser
327          180         185         190
330 Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile
331          195         200         205
334 Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp
335          210         215         220
338 Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe
339 225         230         235         240
342 Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser
343          245         250         255
346 Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu
347          260         265         270
350 Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly
351          275         280         285
354 Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe
355          290         295         300
358 Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu

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359 305          310          315          320
362 Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe
363          325          330          335
366 Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg
367          340          345          350
370 Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu
371          355          360          365
374 Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr
375          370          375          380
378 Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu
379 385          390          395          400
382 Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu
383          405          410          415
W--> 386 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
387          420
390 <210> SEQ ID NO: 5
391 <211> LENGTH: 602
392 <212> TYPE: DNA
393 <213> ORGANISM: Mycoplasma hyopneumoniae
395 <400> SEQUENCE: 5
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398 aacgcatcac cgtgttgaaa accagaaagt actcaaacat ttttggtggt attagcaagt 120
400 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctoca 180
402 gtaagagcgc caagttggtg aattgcctct caacttgatt gggttaaata attatcattt 240
404 accgttccac cagcgggttac aattgccata tttagcccaa aatgtttggt tgcacagct 300
406 tttgcggcca taatttcgga ttttcgttca ttaactagtc ctgaaatttt tgagacatca 360
408 gtgatttgct tatttttgatt atcggctgat ttttcttctt tagttgtttc tttatcccaa 420
410 catccggcag agattgtcgc gattgtctgaa agcggaaaaa ctaagcctaa gccagaataa 480
412 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattgttt taattacgat 540
414 gactttcaat tatttttttaa taaattaatt tttattttac attttctatt atattcaaaa 600
416 ac 602
419 <210> SEQ ID NO: 6
420 <211> LENGTH: 200
421 <212> TYPE: PRT
422 <213> ORGANISM: Mycoplasma hyopneumoniae
424 <400> SEQUENCE: 6
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427 1          5          10          15
430 Asn His Leu Val Asn Ala Ser Pro Cys Trp Lys Pro Glu Ser Thr Gln
431          20          25          30
434 Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser
435          35          40          45
438 Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro
439          50          55          60
442 Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe
443 65          70          75          80
446 Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu
447          85          90          95
450 Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/14/2003
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Input Set : A:\3153.162.PC10555A.Substitute.Seq.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 417,418,419,420,421,422,423

Seq#:7; Xaa Pos. 3

Seq#:10; N Pos. 9,18,21

Seq#:12; N Pos. 6,9,12,18,21,24

Seq#:14; N Pos. 4,7,10,16,19,22